

seq ID NO: 1

Database : GenEmbl:*

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- 8: gb_sy:*
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- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
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	2	1134	100.0	3104	2	AX615036	<i>rm</i>	AX615036	Sequence
	3	1134	100.0	3104	15	SPU45308	<i>bad class</i>	U45308	Synechococc
	4	1134	100.0	110000	15	CP000100_05	<i>bad date</i>	Continuation (6 of	
c	5	1134	100.0	110000	15	AP008231_10	<i>bad date</i>	Continuation (11 o	
c	6	503.6	44.4	110000	15	BA000039_04		Continuation (5 of	
	7	485.6	42.8	110000	15	BA000022_23		Continuation (24 o	
c	8	485	42.8	110000	15	CP000239_10		Continuation (11 o	
	9	466	41.1	110000	15	CP000240_24		Continuation (25 o	

Database : Published_Applications_NA_Main:*

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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Query Match	Length			
1	485.6	42.8	1230	7	US-10-369-493-26469	Sequence 26469, A
2	466.2	41.1	1107	7	US-10-369-493-43685	Sequence 43685, A
3	161.4	14.2	1785	8	US-10-437-963-75871	Sequence 75871, A
4	161.4	14.2	2065	8	US-10-424-599-18773	Sequence 18773, A
5	147.4	13.0	1879	8	US-10-424-599-18772	Sequence 18772, A
6	140.6	12.4	1716	8	US-10-767-701-8981	Sequence 8981, Ap
7	133.4	11.8	1949	8	US-10-425-114-30648	Sequence 30648, A
8	133.4	11.8	2077	9	US-10-425-115-47612	Sequence 47612, A
9	133.2	11.7	1295	9	US-10-425-115-52894	Sequence 52894, A

Database : Published_Applications_NA_New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	161.4	14.2	1633	6	US-10-449-902-2362	Sequence 2362, Ap
c 4	150.4	13.3	1950	7	US-11-218-305-5034	Sequence 5034, Ap
5	146	12.9	1908	8	US-11-216-545-1060	Sequence 1060, Ap
6	142.4	12.6	2131	6	US-10-449-902-15521	Sequence 15521, A
7	133.4	11.8	2850	7	US-11-218-305-18858	Sequence 18858, A
c 8	125.2	11.0	1314	7	US-11-218-305-24484	Sequence 24484, A
c 9	124.6	11.0	1927	7	US-11-218-305-24482	Sequence 24482, A
10	123	10.8	2031	6	US-10-449-902-7919	Sequence 7919, Ap
11	122.8	10.8	1294	6	US-10-449-902-3517	Sequence 3517, Ap
c 12	121.4	10.7	1666	7	US-11-218-305-24483	Sequence 24483, A
c 13	121	10.7	1921	7	US-11-218-305-24481	Sequence 24481, A
c 14	80	7.1	775	8	US-11-266-748A-80959	Sequence 80959, A
15	80	7.1	775	8	US-11-266-748A-133770	Sequence 133770,
16	54.8	4.8	389	7	US-11-218-305-5732	Sequence 5732, Ap
c 17	41.6	3.7	5178	6	US-10-537-017-2	Sequence 2, Appli
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RESULT 3
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 VERSION U45308.2 GI:6492404
 KEYWORDS .
 SOURCE Synechococcus elongatus PCC 7942
 ORGANISM Synechococcus elongatus PCC 7942
 Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 REFERENCE 1 (bases 1 to 1953)
 AUTHORS Guler,S., Seeliger,A., Hartel,H., Renger,G. and Benning,C.
 TITLE A null mutant of Synechococcus sp. PCC7942 deficient in the sulfolipid sulfoquinovosyl diacylglycerol
 JOURNAL J. Biol. Chem. 271 (13), 7501-7507 (1996)
 PUBMED 8631780
 REFERENCE 2 (bases 1596 to 3104)
 AUTHORS Guler,S., Essigmann,B. and Benning,C.
 TITLE A cyanobacterial gene, sqdX, required for biosynthesis of the sulfolipid sulfoquinovosyldiacylglycerol
 JOURNAL J. Bacteriol. 182 (2), 543-545 (2000)
 PUBMED 10629209
 REFERENCE 3 (bases 1 to 1953)
 AUTHORS Benning,C. and Guler,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-1996) IGF Berlin, Ihnestr. 63, Berlin 14195, Germany
 REFERENCE 4 (bases 1 to 3104)
 AUTHORS Guler,S., Essigmann,B. and Benning,C.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1999) Dept. of Biochemistry, Michigan State University, East Lansing, MI 10117, USA
 REMARK Sequence update by submitter
 COMMENT On Dec 1, 1999 this sequence version replaced gi:1177752.
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CDS

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ORIGIN

Query Match 100.0%; Score 1134; DB 15; Length 3104;
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Qy	1	ATGCGCATCGCTCTCTTTACCGAGACGTTCTCCCCAAAGTGGATGGCATCGTCACGCGG	60
Db	1800	ATGCGCATCGCTCTCTTTACCGAGACGTTCTCCCCAAAGTGGATGGCATCGTCACGCGG	1859
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Db	2100	TACTATGCCAAGGCGCTAAATGTGCCACTCGTGGCGTCCTATCACACCCATTTGCCGAAA	2159
Qy	361	TACCTTGAGCATTACGGGCTGGGGGTCTTGGAGGGGGTGCTCTGGGAATTGCTGAAGCTG	420
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Qy	661	TTGGATGCCAATCCTGAGGCTTGCTTGGCCTTGGTCGGCGATGGCCCGCATCGGGCCGAA	720
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Db	2520	CTAGAGCAATTGTTTGTCTGGCACCCAGACGCAGTTTATTGGCTATCTGCATGGGGAACAG	2579
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Db	2580	CTAGGGGCGGCCTACGCTTCTGCTGACGCTTTTGTCTTTCCCTCCCGGACCGAAACCCTC	2639
Qy	841	GGTCTAGTCTTGCTGGAAGCCATGGCAGCGGGTTGTCCGGTCGTGGCGGCCAATTCCGGT	900
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Qy	901	GGCATTCCCGATATTGTCAGCGACGGCATTAATGGTTTCTGTTTCGATCCTGAGGATGAA	960
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Qy	1081	CAGGACTACTACTGCGAGGTGTTGGCAGATGGTTGCTTACCCTTAGCGGCCTGA	1134
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Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
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- 11: geneseqn2003ds:*
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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1134	100.0	1134	6	ABQ75827			Abq75827 Cyanobact
	2	485.6	42.8	1230	13	ADS48039			Ads48039 Bacterial
	3	466.2	41.1	1107	13	ADT45247			Adt45247 Bacterial
	4	161.4	14.2	1633	14	AEB67217			Aeb67217 Rice geno
	5	144.8	12.8	1533	6	ABQ81780			Abq81780 Arabidops
	6	133.4	11.8	1949	13	ADX59805			Adx59805 Plant ful
c	7	126	11.1	615	9	ACL17706			Acl17706 DNA clone
	8	124.4	11.0	1244	13	ADX63809			Adx63809 Plant ful
c	9	120.4	10.6	619	9	ACL17711			Acl17711 DNA clone
	10	119.2	10.5	1344	14	AED46770			Aed46770 Membrane
c	11	117.8	10.4	569	9	ACL17707			Acl17707 DNA clone
	12	117.6	10.4	1221	8	ACA02161			Aca02161 C. glutam

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
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- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	96.6	8.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli	
4	91.6	8.1	1341	3	US-09-252-991A-12827	Sequence 12827, A	
5	64	5.6	1326	3	US-09-328-352-4064	Sequence 4064, Ap	
6	63	5.6	714	3	US-09-252-991A-5165	Sequence 5165, Ap	
c 7	63	5.6	1251	3	US-09-252-991A-5016	Sequence 5016, Ap	
8	63	5.6	1584	3	US-09-252-991A-5109	Sequence 5109, Ap	
9	60.8	5.4	1032	3	US-09-902-540-6426	Sequence 6426, Ap	
10	60.8	5.4	2632	3	US-09-902-540-440	Sequence 440, App	
11	60.6	5.3	690	3	US-09-252-991A-12684	Sequence 12684	

Database : EST:*

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- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query	DB			
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c	3	146.4	12.9	922	10	DT505119			DT505119 WS01810.C
c	4	142.6	12.6	961	10	DT518735			DT518735 WS02439.B
	5	141.8	12.5	785	9	DN620750			DN620750 UCRCS11_0
c	6	139.8	12.3	791	10	DV105721			DV105721 chiou0021
	7	139.6	12.3	904	10	DV711665			DV711665 CGN-60518
	8	136.4	12.0	887	8	CO364415			CO364415 RTK1_15_C
	9	136.2	12.0	643	2	BJ258639			BJ258639 BJ258639
	10	132.2	11.7	532	5	CF196703			CF196703 Ir64bi1.6
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Seq ID NO:3

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
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- 6: gb_ro:*
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- 8: gb_sy:*
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- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	2979	100.0	2979	2	AX615031		AX615031	Sequence
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	3	507.2	17.0	554	8	ATH506242		AJ506242	Arabidops
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c	5	350.6	11.8	1533	4	AF454354		AF454354	Arabidops
c	6	350.6	11.8	1564	4	BT005796		BT005796	Arabidops
c	7	281	9.4	1503	4	AY045961		AY045961	Arabidops
c	8	166	5.6	600	8	ATH506241		AJ506241	Arabidops
c	9	137.2	4.6	134390	4	CT030165		CT030165	M.truncat
c	10	136.6	4.6	1822	4	BT014103		BT014103	Lycopersi
c	11	136.4	4.6	110000	4	AP008207_022		Continuation (23 o	
c	12	136.4	4.6	167405	4	AP002483		AP002483	Oryza sat
c	13	136.4	4.6	175565	4	AP003311		AP003311	Oryza sat
c	14	135.8	4.6	39990	4	AP008222		AP008222	Oryza sat
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Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	2979	100.0	2979	6	ABQ75828			Abq75828 Arabidops
c	2	350.6	11.8	1533	6	ABQ81780			Abq81780 Arabidops
c	3	145	4.9	972	13	ADO81288			Ado81288 Plant ful
c	4	145	4.9	1949	13	ADX59805			Adx59805 Plant ful
c	5	134.2	4.5	651	13	ADX12835			Adx12835 Plant ful
c	6	133.8	4.5	1633	14	AEB67217			Aeb67217 Rice geno
	7	132.4	4.4	569	9	ACL17707			Acl17707 DNA clone
	8	132.4	4.4	615	9	ACL17706			Acl17706 DNA clone

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				ID	Description
	No.	Score	Match	Length	DB					
c	1	78.4	2.6	174	3	US-09-313-294A-5690				Sequence 5690, Ap
c	2	63	2.1	7218	2	US-08-232-463-14				Sequence 14, Appl
	3	60	2.0	612	3	US-09-902-540-1357				Sequence 1357, Ap
c	4	60	2.0	4403765	3	US-09-103-840A-2				Sequence 2, Appli
c	5	60	2.0	4411529	3	US-09-103-840A-1				Sequence 1, Appli
c	6	59.6	2.0	1141	3	US-09-806-708B-22				Sequence 22, Appl
	7	54.8	1.8	1039	3	US-09-902-540-1280				Sequence 1280, Ap
	8	52	1.7	1141	3	US-09-806-708B-22				Sequence 22, Appl
	9	48.6	1.6	7218	2	US-08-232-463-14				Sequence 14, Appl
c	10	48	1.6	23849	3	US-09-949-016-13813				Sequence 13813, A
c	11	47.4	1.6	1326	3	US-09-328-352-4064				Sequence 4064, Ap
	12	47.4	1.6	2604	3	US-09-839-894-5				Sequence 5, Appli

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Query Match	Length	DB			
	1	416	14.0	866	11	BH468052	BH468052	BOHOJ24TF
	2	383.6	12.9	1279	14	AJ855270	AJ855270	Brassica
c	3	339.6	11.4	1725	6	CNS0A253	BX830044	Arabidops
c	4	324	10.9	806	11	BZ452202	BZ452202	BONOA48TR
	5	318.2	10.7	747	11	BH947656	BH947656	obu80c04.
c	6	313.6	10.5	361	11	BH849950	BH849950	SALK_0705
	7	301	10.1	301	11	BH904697	BH904697	

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	Query	Match	Length	DB	ID		
No.	Score						
c	1	153.4	5.1	2065	8	US-10-424-599-18773	Sequence 18773, A
c	2	150.4	5.0	2033	8	US-10-424-599-70595	Sequence 70595, A
c	3	145	4.9	972	8	US-10-425-114-8	Sequence 8, Appli
c	4	145	4.9	1949	8	US-10-425-114-30648	Sequence 30648, A
c	5	145	4.9	2077	9	US-10-425-115-47612	Sequence 47612, A
c	6	143.8	4.8	1879	8	US-10-424-599-18772	Sequence

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB			
c	1	155	5.2	2093	8	US-11-216-545-1059		Sequence 1059, Ap
c	2	150.4	5.0	1908	8	US-11-216-545-1060		Sequence 1060, Ap
c	3	145	4.9	2850	7	US-11-218-305-18858		Sequence 18858, A
c	4	134.4	4.5	1294	6	US-10-449-902-3517		Sequence 3517, Ap
c	5	134.4	4.5	2131	6	US-10-449-902-15521		Sequence 15521, A
c	6	133.8	4.5	1606	6	US-10-449-902-22084		Sequence 22084, A
c	7	133.8	4.5	1633	6	US-10-449-902-2362		Sequence 2362, Ap
	8	133.8	4.5	1950	7	US-11-218-305-5034		Sequence 5034, Ap
c	9	133.2	4.5	2031	6	US-10-449-902-7919		Sequence 7919, Ap
	10	129.4	4.3	1921	7	US-11-218-305-24481		Sequence 24481, A
	11	126.4	4.2	1314	7	US-11-218-305-24484		Sequence 24484, A
	12	124.8	4.2	1666	7	US-11-218-305-24483		Sequence 24483, A

Seq ID 10: 6

Database : GenEmbl:*

- 1: gb_env:*
- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Query Match Length	DB	ID	
1	1799	100.0	1799	2	AX615033	AX615033 Sequence
2	1799	100.0	1799	2	AX615034	AX615034 Sequence
3	1799	100.0	1799	4	AF022082	AF022082 Arabidops
4	1718	95.5	1797	4	AF380641	AF380641 Arabidops
5	1546.2	85.9	94482	4	ATF26P21	AL031804 Arabidops
6	1546.2	85.9	111876	4	ATF4I10	AL035525 Arabidops
7	1546.2	85.9	198669	4	ATCHRIV78	AL161582 Arabidops
8	1434	79.7	1434	2	CQ805256	CQ805256 Sequence
9	1434	79.7	1434	4	AY113071	AY113071 Arabidops
10	803.8	44.7	1843	4	AY192559	AY192559 Spinacia
11	747.8	41.6	2060	4	AK065310	AK065310 Oryza sat
12	746.2	41.5	2233	4	AK060744	AK060744 Oryza sat
c 13	586.4	32.6	99567	12	AP007324	AP007324 Lotus cor
14	573.4	31.9	111256	4	AC125478	AC125478 Medicago

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1799	100.0	1799	6	ABQ81781	Abq81781 Arabidops
2	1434	79.7	1434	12	ADN73772	Adn73772 Thale cre
3	746.2	41.5	2233	14	AEB67817	Aeb67817 Rice geno
4	519.4	28.9	1143	13	ADT45246	Adt45246 Bacterial
5	505	28.1	1143	13	ADT43979	Adt43979 Bacterial
6	477.4	26.5	1152	13	ADS47906	Ads47906 Bacterial
7	360.6	20.0	572	13	ACN59093	Acn59093 Cotton gy
8	232	12.9	1152	13	ADS61520	Ads61520 Bacterial
9	215.8	12.0	1170	13	ADT43484	Adt43484 Bacterial
10	185.4	10.3	1137	13	ADS58925	Ads58925 Bacterial
11	160	8.9	1212	13	ADS56061	Ads56061 Bacterial
12	144.4	8.0	1182	13	ADT46275	Adt46275 Bacterial
13	143.4	8.0	248	7	ADS66523	Ads66523 Corn seed
14	141.4	7.9	1209	6	ABQ81782	Abq81782

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	46.2	2.6	362	3	US-09-621-976-16509	Sequence 16509, A
2	45	2.5	2915	3	US-09-578-063-72	Sequence 72, Appl
3	45	2.5	2915	5	US-09-333-159-72	Sequence 72, Appl
4	44.4	2.5	2369	3	US-09-057-996-13	Sequence 13, Appl
5	43.4	2.4	1412	3	US-09-614-912-197	Sequence 197, App
6	43	2.4	3338	3	US-09-489-847-117	Sequence 117, App
7	43	2.4	4244	3	US-09-620-312D-151	Sequence 151, App
8	42.6	2.4	1081	3	US-09-372-422A-33	Sequence 33, Appl
c 9	42.4	2.4	611	3	US-09-385-982-70	Sequence 70, Appl
10	42.4	2.4	2830	3	US-09-646-561-25	Sequence 25, Appl

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Query	Match	Length				
	1	1727.2	96.0	1806	6	CNS0A2S1			BX827511 Arabidops
	2	1676.4	93.2	1744	6	CNS0A3AQ			BX826685 Arabidops
	3	1634.2	90.8	1717	6	CNS0A2TO			BX827393 Arabidops
	4	835.2	46.4	953	4	BX836978			BX836978 BX836978
	5	722.8	40.2	803	4	BX836994			BX836994 BX836994
	6	704	39.1	705	7	AV821229			AV821229 AV821229
	7	703.8	39.1	709	4	CB255030			CB255030 52-E01533
	8	696.8	38.7	717	10	DR365949			DR365949 11057256
	9	661	36.7	661	10	DR365956			DR365956 11070500
	10	625.2	34.8	675	9	DR233193			DR233193 12847581
c	11	597	33.2	685	7	AV781569			AV781569

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	833.6	46.3	2017	8	US-10-424-599-32730	Sequence 32730, A	
2	719.8	40.0	1910	9	US-10-425-115-46347	Sequence 46347, A	
3	519.4	28.9	1143	7	US-10-369-493-43684	Sequence 43684, A	
4	505	28.1	1143	7	US-10-369-493-42417	Sequence 42417, A	
5	493.2	27.4	1405	8	US-10-437-963-22989	Sequence 22989, A	
6	477.4	26.5	1152	7	US-10-369-493-26336	Sequence 26336, A	
7	406.6	22.6	1119	8	US-10-767-701-10375	Sequence 10375, A	
8	360.6	20.0	572	8	US-10-021-323-13874	Sequence 13874, A	
c 9	306	17.0	925	8	US-10-767-701-7240	Sequence 7240, Ap	
10	232	12.9	1152	7	US-10-369-493-37194	Sequence 37194, A	

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	747.8	41.6	2060	6	US-10-449-902-14764	Sequence 14764, A
2	746.2	41.5	2233	6	US-10-449-902-2962	Sequence 2962, Ap
3	716.6	39.8	1882	7	US-11-218-305-3418	Sequence 3418, Ap
4	529.4	29.4	3248	7	US-11-218-305-3416	Sequence 3416, Ap
5	500.2	27.8	1124	6	US-10-449-902-3777	Sequence 3777, Ap
6	500.2	27.8	1124	6	US-10-449-902-4194	Sequence 4194, Ap
7	46.4	2.6	627	8	US-11-266-748A-52757	Sequence 52757, A
8	46.4	2.6	627	8	US-11-266-748A-209159	Sequence 209159,
9	46	2.6	857	8	US-11-216-545-545	Sequence 545, App
10	45.8	2.5	3720	8	US-11-266-748A-28319	Sequence 28319, A
11	45.2	2.5	1000	8	US-11-266-748A-283925	Sequence 283925,
c 12	45.2	2.5	1000	8	US-11-266-748A-335354	